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OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 02:55:20 ; Search time 3610 Seconds

(without alignments)  
16179.870 Million cell updates/sec

Title: US-09-716-536-7

Perfect score: 2007

Sequence: 1 gtcggtgagcgaattg.....aaaaaaaaaaaaaaaaa 2007

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba:\*

2: gb\_bt:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

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9: gb\_pr:\*

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11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

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18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

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32: em\_htg\_other:\*

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35: em\_htg\_rnd:\*

36: em\_htg\_mam:\*

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40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	1890.8	94.2	2005	6	AR072729
6	1890.8	94.2	2005	6	BD006990
7	1087	54.2	2024	10	BC017374
8	1081	53.9	1981	10	MMU77844
9	1062.8	53.0	1975	6	AR193168
10	892.8	44.5	1781	6	AX364873
11	521.6	26.0	3694	10	BC006929
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#### ALIGNMENTS

RESULT 1

AR193167

LOCUS AR193167

DEFINITION Sequence 7 from patent US 6346605.

ACCESSION AR193167

VERSION AR193167.1 GI:20239132

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2007)

AUTHORS Lee,S.Young, and Choi,Y.

TITLE Signal Transducer for the TNF receptor super family, and uses thereof

JOURNAL Patent: US 6346605-A 7 12-FEB-2002;

FEATURES Location/Qualifiers  
source 1..2007  
BASE COUNT 517 a 518 c 558 g 414 t  
ORIGIN

Query Match 100.0%; Score 2007; DB 6; Length 2007;  
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Matches 2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION   U77845
VERSION     U77845.1  GI:2039303
KEYWORDS
SOURCE      Homo sapiens.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2007)
AUTHORS     TRAF-Interacting protein (TRIP): a novel component of the tumor
            necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes
            that inhibits TRAF2-mediated NF-kappaB activation
            Lee,S.Y., Lee,S.Y. and Choi,Y.
            J. Exp. Med. 185 (7), 1275-1285 (1997)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 2010)  
 AUTHORS Strausberg, R.  
 JOURNAL Direct Submission  
 Submitted (15-Nov-2000) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
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 Email: c9apbs-rt@mail.nih.gov  
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 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,  
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,  
 Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McKloskey, J.C.,  
 McDowell, J., Pearson, R., Snyder, B., Stantirpop, S., Thomas, P.J.,  
 Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,  
 Zhang, L.-H. and Green, E.D.



QY	1635	GTGAGGATGAGTGTGGGACACCCAGAGACACTGCTCTTCCCTGACCCTCCACCTCCGCACTCTA	1694
QY	1699	CGACTGGGAGGCTGACATGACCGACCCACTGATCCTGTGACGAGGTCTGCT -CTGTGGC	1757
Db	1695	CGACTGGGAGGCTGACATGACCGACCCACTGATCCTGTGACGAGGTCTGCTGTGGC	1754
QY	1758	AGGCTCTGTGTTATATAGCCATGATCAGATGTGGTCAAGACTCTTCTTGGGCTTGGAACCAAC	1817
Db	1755	AGGCTCTGTGTTATATAGCCATGATCAGATGTGGTCAAGACTCTTCTTGGGCTTGGAACCAAC	1814
QY	1818	GGTCACTGTTTACAGTCTCTCTGTGGACCAAGATGCTTGAGGATATCCAGGCGCCTCAAGC	1877
Db	1815	GCTCACTGTTTACAGTCTCTCTGTGGACCAAGATGCTTGAGGATATCCAGGCGCCTCAAGC	1874
QY	1878	CCAACTCTTCTACCTGCTCTTGTGACTGCTTCTTA -GCATAGCCTGGGCCAAAGCAGGTGGGG	1936
Db	1875	CCAACTCTTCTACCTGCTCTTGTGACTGCTTCTTAAGCATATAGCCTGGGCCAAAGCAGGTGGGGT	1934
QY	1937	AATGAGATGATGACATGGGATGTATGAGAGAGATGGAAAGATTTTCCGAAAAAATAA	1996
Db	1935	AATGAGATGATGACATGGGATGTATGAGAGAGATGGAAAGATTTTCTATGATTAATAATTT	1993
QY	1997	AAAAAAAAAAAA 2007	
Db	1994	AAAAAAAAAAAA 2004	
RESULT 5	AR072729		
LOCUS	AR072729	2065 bp	DNA linear PAT 28-AUG-2000
DEFINITION	Sequence 1 from patent US 5948643.		
ACCESSION	AR072729		
VERSION	AR072729.1	GI:999493	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2065)		
JOURNAL	Rubinfeld,B., Polakis,P.G., Ingenfelder,C. and Vuong,T.T.		
FEATURES	Modulators of BRCA1 activity		
	Patent: US 5948643-A 1 07-SEP-1999;		
	Location/Qualifiers		
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BASE COUNT	561 a 526 c 561 g 417 t		
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Query Match	94.2%; Score 1890.8; DB 6; Length 2065;		
Best Local Similarity	98.9%; Pred. No. 0;		
Matches 1946; Conservative	0; Mismatches 17; Indels 5; Gaps 4;		
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QY	224	CACCAAGTCGAGCCTGCGCCACAGTCCGCAATCCAGTTGGCAAAAGAACATTATCAATA	283
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QY	284	AGCTCTTCTTTGATCTTGGCCAGAGAGAGAAATGCTTTGGATCGAGAAATCTTAAAGA	343
Db	284	AGCTCTTCTTTGATCTTGGCCAGAGAGAGAAATGCTTTGGATCGAGAAATCTTAAAGA	343
QY	344	ATGAACGTGACATGTCAAGCCCAAGCTTTCCCAAGAAACAAGAGAAAGACAGACGC	403

Db	344	ATGAACGTGGACATGTCTCAGAGCCACCTTTCCAGAAAGACAGAGAAACGACACACC	403
QY	404	AGGTCATCATCTGACACTCTCGGGATACGCTGGAAAGACGCATCTACTGTGATCTC	463
Db	404	AGGTCATCATCTGACACTCTCGGGATACGCTGGAAAGACGCATCTACTGTGATCTC	463
QY	464	TGCAGCAGGCTTTGGCCAGGCGGAGATGCTGTCTCCACTGAAAAAGCAGATGAAGT	523
Db	464	TGCAGCAGGCTTTGGCCAGGCGGAGATGCTGTCTCCACTGAAAAAGCAGATGAAGT	523
QY	524	ACTTAGAGCAGCACCAGAGTAGAGACCAACAAACAGACAAAGAGAGGCGGGCCGCTCAGA	583
Db	524	ACTTAGAGCAGCACCAGAGTAGAGACCAACAAACAGACAAAGAGAGGCGGGCCGCTCAGA	583
QY	584	GCAAGATGAAGACCATGAGACAGATTGAGCTTCTACTCAGAGCCAGGCTCCGTGAGTGG	643
Db	584	GCAAGATGAAGACCATGAGACAGATTGAGCTTCTACTCAGAGCCAGGCTCCGTGAGTGG	643
QY	644	AGGAGATGATCCGAGACATGGTGTGGGACGTACAGGGGTGAACAGCTGGCTGTGTACT	703
Db	644	AGGAGATGATCCGAGACATGGTGTGGGACGTACAGGGGTGAACAGCTGGCTGTGTACT	703
QY	704	GTGTCCTCTCAAAAGAGTACGAGATCTTAAAGAGGACGGAAGGCTCTCAGGGGAGG	763
Db	704	GTGTCCTCTCAAAAGAGTACGAGATCTTAAAGAGGACGGAAGGCTCTCAGGGGAGG	763
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QY	824	CTGAATTGGATCAGGCCAAGTTAGAACGTGAAGTCAGCCCGAAGGACATTACAGAGTGTG	883
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QY	884	ACAAGGAATATCATGAGCTCTAAAAAGAGCTAACATGCTCGACAGAAACTTTGAACCTGC	943
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QY	1184	GGAAGAGTCCACAGCTCTCACTGGGTGGCCAGAGCTGTGACGAGAGAGCCAGATGTGAGAAC	1243
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QY	1244	TGTGTTGGTCTCTCCCTAATTTTGTCTCGGATGCCATCTTAGGCCAGAAACGCCAAGA	1303
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QY	1304	GGCCAGGTCTGAGTCTCTTTGACGCAAAATGTGTTAAGAGACAGGCTTCGATGGGGCTCG	1363
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QY	1364	GTGGCGGACAAATTTCAATCAGCTACTGACAGTCAATGATCCGCCATTTGCCCTGTTA	1423
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QY	1424	AGCCCAAGACCAAGTTAAGCAGAGGGTGAAGGCTGTAAGACCGTCCCTCTCTTCTTCAGG	1483
Db	1424	AGCCCAAGACCAAGTTAAGCAGAGGGTGAAGGCTGTAAGACCGTCCCTCTCTTCTTCAGG	1483



QY 1484 CCAAGCTGGACACCTTCTGTCGTGAGAACAGTGTGACCAATGGCCAGACACA 1543  
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Db 1484 CCAAGCTGGACACCTTCTGTCGTGAGAACAGTGTGACCAATGGCCAGACACA 1543  
QY 1544 TGCCTGCAACTGTAGTCAAGACAGTGTCCAGGACAGG--TTTGTGACAGACCTTACT 1601  
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LOCUS BD006990 2065 bp DNA linear PAT 31-JAN-2002  
DEFINITION Modulators of BRCA1 activity.  
ACCESSION BD006990  
VERSION BD006990.1 GI:18635361  
KEYWORDS JP 2001502893-A/1.  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2065)  
AUTHORS Lubinfield, B., Porakitsu, P., Rigenferuta, C. and Buon, T. T.  
TITLE Modulators of BRCA1 activity  
JOURNAL Patent: JP 2001502893-A 1 06-MAR-2001;  
ONIX PHARMACEUTICALS INC

COMMENT OS Unidentified  
PN JP 2001502893-A/1  
PD 06-MAR-2001  
PF 06-AUG-1997 JP 1998512659  
PI 04-SEP-1996 US 60/025601  
PI BONY LUBINFELD, PAUL, PORAKITSU, CAROL, RIGENFERUTA, TERIRIN T, BUON  
PC C12N15/09, A61K38/00, A61P43/00, C07K14/435, C07K16/18, C12N1/15,  
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FH key Location/Qualifiers  
FT CDS Location/Qualifiers  
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BASE COUNT 561 a 526 c 561 g 417 t  
ORIGIN

Query Match 94.2%; Score 1890.8; DB 6; Length 2065;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1946; Conservative 0; Mismatches 17; Indels 5; Gaps 4;  
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[illegible]

RESULT 7	BC017374	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
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BC017374	IMAGE:3990371, mRNA, complete cds.					
BC017374.1	GI:16924208					
MGC:						

REFERENCE	AUTHORS	JOURNAL	TITLE
1	(bases 1 to 2024)	Strausberg, R.	Direct Submission
2			Submitted (13-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
3			NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
4			Contact: MGC help desk
5			Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a>
6			Tissue Procurement: Gilbert Smith, Ph.D.
7			cDNA Library Preparation: Life Technologies, Inc.
8			cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
9			DNA Sequencing by: Institute for Systems Biology
10			<a href="http://www.systemsbio.org">http://www.systemsbio.org</a>
11			contact: <a href="mailto:amadane@systemsbiology.org">amadane@systemsbiology.org</a>
12			Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting
13			Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
14			Series: IRAC Plate: 18 Row: 5
15			This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755868.
16			Location/Qualifiers
17			1. 2024
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19			/db_xref="taxon:10090"
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22			/tissue_type="Mammary tumor metastasized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMV."
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30			/db_xref="GI:16924209"
31			/db_xref="locusid:22036"
32			/translation="MPRIATCTCSDFPDSRDVAIHCGRTHLLOLIMEFAPSR
33			TCPCRIOVGKRTIINKFLDLAEENVDIAEELKNELDVSVKQLSQDEKEDSDQA
34			IIDPLRDLERNAIVESLONALKAELNCSLEKQKPFLEQRODERKQAEKEDSDQA
35			CKMTMDQIELLLQSOREVEDEMRDGVGSAVEOLAIVCVSLKFEYENLKEARLAK
36			GELMDRLKDLVSSRSRLKLTUNTELDQALELRSQKDLSDADELSRLKMLILOG
37			TLSPATNEVSRVLESPSPAPVEMNPMLRPLHVGPGEDIDNTEVDVPTPTSGSD
38			HCILPKILCFERASPMONVILKKVHKVSPRESLSLGQRCGELDELAACPLFIEN
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41			BASE COUNT
42			582 a 489 c 528 g 425 t
43			ORIGIN
44			Query Match
45			54.2% Score 1087; DB 10; Length 2024;
46			Best Local Similarity 74.9%; Freq. No. 9.5e-296;
47			Matches 1492; Conservative 0; Mismatches 440; Indels 61; Gaps 8;
48			26 AGCGAGGCGGGCGCTCAGCAAGCCGAGACTGTAGACAGTTCTTGGCTCGTGGGCC 85
49			
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51			CGTTAGTTCAGCAGCATCATCCCTATCCGTCTGTCTGTGACATATCTGTCGACTTCTTCG 145
52			
53			Db GCTTGAGTGAGCAGCATTCAGCTATTCGGGGCTCTGTGACATATCTGTCGACTTCTTCG 144
54			ATCACTCCCGGAGCTGGCGCGCAGATTCACATGGCGGCAACACTTTCGACATGGAGTGCCTAA 205
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Db	205	TTCCAGTGGTTTGAGACAGACCAAAGTCGACCTGCCACCAGATGCGGAATCCAGGTTGGCA	264
OY	266	AAAGACCATTAATCAATTAAGCTCTCTTTGATGTCGACGAGGAGGAGGAAATGCTTGG	325
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OY	326	ATCGAAGATTTCTTAAAGAAATGAACGTGACAAATGTCAGAGGCCAGCTTTCCAGAAAGACA	385
Db	325	ATCGAAGATTTCTTAAAGAAATGAACGTGACAGCGCTCAAGAGCTGAGCTTTCCAGAAAGACA	384
OY	386	AGGAGAAACGAGACAGCCAGCTATCATCTGACACTCTGGCGGATTAAGCTGGAAGAACGA	445
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OY	446	ATGCTACTGTGGTATTCCTCTGACAGAGCCCTTGGGGCAAGGCCGAGATGCTGCTCCACAC	505
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OY	506	TGAAAAAGCAGATGAATACTTAGAGACGACGAGATGAGACCAACAAGACAAAGAG	565
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Db	625	GCCAGCGGTGTGAGGTGGAGAGATGATTCGACACATGGGTGGGACAGTCACCGGTGG	684
OY	686	AACAGCTGGCTGTACTGTGTGTCTCTCAAGAAAGATGACGAATCTTAAAGAGGGCAC	745
Db	685	AGCAGCTGGCTGTACTGTGTGTCTCTCAAGAAAGATGATGAAATCTTGAAGAGAGCTC	744
OY	746	GGAAGCCCTCAGGGAGGTGGCTGACAAAGCTGAGAGGAATTTGTTTCTCTCCAGAGCA	805
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OY	806	AGTTGCGACAGCTACTCTGTAANTTGATTCAGGCCAAATTGAACACTGAAGTCAGCCACA	865
Db	805	AGTTGAGACACTCTCAACACTGAGCTGATCAAGGCCAAATTGAACACTGAAGTCAGCCACA	864
OY	866	AGGACTTACAGATGCTGACAAAGGAATCATGAGCCCTGAAAAAAGACATCAAGATGCTGC	925
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OY	926	AGGAAACCTTGAACCTGCCACACAGTGGCCACGTAGACTGCAACGGCTGTGTTTTAGAGA	985
Db	925	AGGAAACCTTGAAGCTCTGCCCGGCGCACANTAGACGGCTGACGCCCTGTGTTTTGAGA	984
OY	986	GCCAGAGCCCTGTGGAGGTG---AATGTGAAGTCCGGCGGCGCATCTTCCTGTGATGA	1042
Db	985	GCCAGAGCCCTGTGGATATGATGACCCGAGGCTTATACCAAGCACCTTCGGTGATGAGA	1044
OY	1043	TTGATCTCAATGCTACTCTTGTGATGTGATATCTCCCAAGCCCGGCGCCTCACTCCAGC	1102
Db	1045	TTGATCTCAATACCACTTGTGATGTAAATCCCTCTCAACCAGACACTCTGTGCTCGACG	1104
OY	1103	ATGATTTACTAGAAAACCTTGGCTGTAGAGAATGACACATGCCCAATTCAGATGTGCCCA	1162
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OY	1163	AGAGATATGCAAAAGGCCCCAGAGAGAGATGCCAGCTCTACATGGGTGGACAGAGCTGTG	1222
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Db	1225	TAGAGAGCTAGATGAGGAACGTGTGTGTCTTCCCTCTTTCATATCCGAATGCTGTGCC	1284

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM
LOCUS	MU077844				
DEFINITION	Mus musculus mTRIP (mTRIP) mRNA, complete cds.				
ACCESSION	U77844.1	GI:2039305			
VERSION					
KEYWORDS					
ORGANISM	Mus musculus.				
	Mus musculus.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1981)				
AUTHORS	Lee,S.Y., Lee,S.Y., and Choi,Y.				
TITLE	TRAF-interacting protein (TRIP): a novel component of the tumor				
	necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes				
	that inhibits TRAF2-mediated NF-kappaB activation				
JOURNAL	J. Exp. Med. 185 (7), 1275-1285 (1997)				
MEDLINE	97258620				
PUBMED	9104814				
REFERENCE	2 (bases 1 to 1981)				

AUTHORS Lee, S.Y., Lee, S.Y. and Choi, Y.  
TITLE Direct Submission  
Submitted (10-NOV-1996) Immunology, The Rockefeller University,  
JOURNAL 1230 York Avenue Box 295, New York, NY 10021, USA  
FEATURES Location/Qualifiers  
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1. 1981  
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BASE COUNT 532 a 489 c 534 g 426 t  
ORIGIN

Query Match 53.9%; Score 1081; DB 10; Length 1981;  
Best Local Similarity 74.6%; Pred. No. 4.7e-294;  
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DB 134 TGTGCACTATCTGCTCCGACTTCTTGATCACTCCCGTACGCTGGCTCACTGCTG 193  
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Db	1705	ATTCACAGGGGCTACTCTCCAGTTGCAGGGGTTTTGGCTTTATAGCTAACACAGGCTGGGCTG	1764
Oy	1793	GACCTTTCTGGGGCTGGAAACACAGCTCACTGTTGATCTGTCCTGGGACAG-----	1847
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Oy	1848	AGTCTTTGAGGCATCTCAGCAGCCTCAGCCCAAGCTTCTACCTGCTTTGACTTGCCTTC	1907
Db	1825	GGATCTCATGAGAGGCTCGAAGACCTCGGCTTGAACTCCTGCTCGCTCCACACTATTGTC	1884
Oy	1908	TAGCATGAGCCGGGCCAAGCAGGAGTGGGGAATGAGCAGTATGAGCATGTATGAGATAG	1967
Db	1885	TGTGAATTTATGGGGTGAGTGGTGATGATAGGGAAGGTGTGGGGAAGTTTCTGTGTAAATA	1944
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LOCUS	AR193168				
DEFINITION	Sequence 8 from patent US 6346605.				
ACCESSION	AR193168				
VERSION	AR193168.1	GI:20239133			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				

Query Match	53.0%	Score 1052.8	DB: 6	Length 1975
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OY	479	GCAAGCGCGAGATCTGTGCTCCACACACTGAAAAAGCAGATGAAATTAAGACAGCAGC	538
Db	488	ACAAAGCAGAGATCTCTGTTCACACCTGAAAAAACAGATGAAGTTCTCGGAGCGAGCGGC	547
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 ACCESSION AX364873  
 VERSION AX364873.1 GI:18696762  
 KEYWORDS

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1  
 AUTHORS Mintz, L., Freilich, S. and Bernstein, J.  
 TITLE Novel nucleic acid and amino acid sequences  
 JOURNAL Patent: WO 0206315-A 24 JAN-2002;  
 Computen Ltd. (IL)  
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Query Match 44.5% Score 892.8; DB 6; Length 1781;  
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REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 129747)  
AUTHORS Wilson, S.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-1999) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
On Mar 7, 1999 this sequence version replaced gi:4176479.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence is the entire insert of clone 465N24. This sequence  
has been finished according to sequence map criteria as follows. An  
attempt is made to resolve all sequencing problems, such as  
compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.

This sequence was generated from part of bacterial clone contigs of  
human chromosome 1, constructed by the Sanger Centre Chromosome 1  
Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr1>  
465N24 is from the library RPC13 constructed at the Roswell Park  
Cancer Institute by the group of Pletier de Jong. For further  
details see <http://pacpac.med.buffalo.edu/VECTOR>.  
pcrPac2.

## FEATURES

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5508. 6164  
repeat\_region  
/note="L1MD1 repeat: matches 5423. .6091 of consensus"  
6176. 6245  
repeat\_region  
/note="35 copies 2 mer ag 67% conserved"  
6247. 6528  
repeat\_region  
/note="AluSg repeat: matches 15. .291 of consensus"  
6529. 6674  
repeat\_region  
/note="73 copies 2 mer ta 73% conserved"  
6741. 6874  
repeat\_region

repeat\_region  
/note="L1MD1 repeat: matches 6090. .6223 of consensus"  
7225. 7278  
repeat\_region  
/note="MIR repeat: matches 36. .85 of consensus"  
8137. 8448  
repeat\_region  
/note="AluX repeat: matches 1. .312 of consensus"  
9092. 9137  
repeat\_region  
/note="23 copies 2 mer at 100% conserved"  
9229. 9326  
repeat\_region  
/note="L2 repeat: matches 2574. .2670 of consensus"  
9669. 9732  
repeat\_region  
/note="MIR repeat: matches 87. .148 of consensus"  
10162. 10365  
repeat\_region  
/note="MIR repeat: matches 8. .222 of consensus"  
10379. 10505  
repeat\_region  
/note="L2 repeat: matches 2586. .2710 of consensus"  
10634. 10814  
repeat\_region  
/note="MER8 repeat: matches 9. .176 of consensus"  
11454. 11752  
repeat\_region  
/note="AluYb repeat: matches 1. .302 of consensus"  
11790. 12171  
repeat\_region  
/note="L1M4 repeat: matches 1258. .1640 of consensus"  
12172. 12362  
repeat\_region  
/note="MER53 repeat: matches 1. .189 of consensus"  
12363. 12775  
repeat\_region  
/note="L1M4 repeat: matches 1640. .2049 of consensus"  
12833. 13130  
repeat\_region  
/note="AluJo repeat: matches 1. .291 of consensus"  
13476. 14035  
repeat\_region  
/note="L1M4 repeat: matches 2224. .2742 of consensus"  
14036. 14330  
repeat\_region  
/note="AluY repeat: matches 1. .301 of consensus"  
14331. 14466  
repeat\_region  
/note="L1M4 repeat: matches 2742. .2867 of consensus"  
14467. 14600  
repeat\_region  
/note="FLAM\_C repeat: matches 1. .133 of consensus"  
14601. 14885  
repeat\_region  
/note="L1M4 repeat: matches 2867. .3278 of consensus"  
14893. 15096  
repeat\_region  
/note="MLTID repeat: matches 286. .505 of consensus"  
15159. 15484  
repeat\_region  
/note="MLTID repeat: matches 6. .323 of consensus"  
15487. 16041  
repeat\_region  
/note="L1MC4 repeat: matches 7451. .7973 of consensus"  
16069. 16773  
repeat\_region  
/note="L1ME3A repeat: matches 3211. .3943 of consensus"  
16774. 17068  
repeat\_region  
/note="AluSg repeat: matches 3. .297 of consensus"  
17071. 17384  
repeat\_region  
/note="AluSg repeat: matches 1. .310 of consensus"  
17385. 17451  
repeat\_region  
/note="L1ME3A repeat: matches 3943. .3955 of consensus"  
17567. 17775  
repeat\_region  
/note="L1ME3A repeat: matches 4012. .4208 of consensus"  
17912. 18219  
repeat\_region  
/note="AluSg repeat: matches 1. .313 of consensus"  
18401. 18922  
repeat\_region  
/note="L1ME3A repeat: matches 4315. .4848 of consensus"  
18923. 19226  
repeat\_region  
/note="AluSg repeat: matches 1. .304 of consensus"  
19227. 19530  
repeat\_region  
/note="L1ME3A repeat: matches 4848. .4586 of consensus"  
19531. 19897  
repeat\_region  
/note="L1PB1 repeat: matches 5781. .6155 of consensus"  
19898. 20698  
repeat\_region  
/note="L1ME3A repeat: matches 4585. .5403 of consensus"  
21061. 21150  
repeat\_region  
/note="MIR repeat: matches 115. .213 of consensus"  
21218. 21390  
repeat\_region  
/note="L2 repeat: matches 1626. .1814 of consensus"  
21511. 21767  
repeat\_region  
/note="L1MC4 repeat: matches 6664. .6940 of consensus"  
21771. 21969  
repeat\_region  
/note="L1MC2 repeat: matches 3850. .4054 of consensus"



```

repeat_region 21970..22008
/Note="U2 repeat: matches 1..39 of consensus"
repeat_region 22009..22354
/Note="LIMC2 repeat: matches 4054..4410 of consensus"
repeat_region 22355..22663
/Note="AlusX repeat: matches 1..309 of consensus"
repeat_region 22664..23340
/Note="LIMC2 repeat: matches 4410..5261 of consensus"
repeat_region 23352..23730
/Note="FAM repeat: matches -135..43 of consensus"
repeat_region 23731..24657
/Note="LIMC2 repeat: matches 5278..6319 of consensus"
repeat_region 24659..24758
/Note="Alu/FLAM repeat: matches 2..77 of consensus"
repeat_region 24759..25029
/Note="LIMC4 repeat: matches 7461..7777 of consensus"
repeat_region 25872..26333
/Note="LIM5 repeat: matches 4828..5368 of consensus"
repeat_region 26334..26622
/Note="LIM8 repeat: matches 5995..6287 of consensus"
repeat_region 26623..26774
/Note="LIM5 repeat: matches 5368..5512 of consensus"
repeat_region 26775..27077
/Note="AlusX repeat: matches 1..298 of consensus"
repeat_region 27078..27856
/Note="LIM5 repeat: matches 5512..6176 of consensus"
repeat_region 27713..27944
/Note="Alu repeat: matches 74..299 of consensus"
repeat_region 27959..28020
/Note="LIM3 repeat: matches 6941..7003 of consensus"
repeat_region 28028..28269
/Note="LIM3 repeat: matches 6941..7003 of consensus"
misc_feature 28146..28221
/Note="121 copies 2 mer 99 60% conserved"
repeat_region 28512..28653
/Note="tandem repeat in single clone region"
repeat_region 29643..30184
/Note="L2 repeat: matches 2241..2422 of consensus"
repeat_region 30368..30450
/Note="L2R2 repeat: matches 1..505 of consensus"
repeat_region 31248..31409
/Note="MIR repeat: matches 28..118 of consensus"
repeat_region 31416..31494
/Note="L2 repeat: matches 1794..1967 of consensus"
/Note="MIR repeat: matches 187..261 of consensus"

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Query Match 13.0%; Score 260; DB 9; Length 129747;

Best Local Similarity 68.4%; Pred. No. 1.2e-61;

Matches 547; Conservative 0; Mismatches 140; Indels 113; Gaps 9;

```

OY 1221 TGCAGAGAGCCAGATGAGGAAGTGGTGGCTTCCCTATTTTGTCCGGAATGCCAT 1280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25030 TTCAATGTGGCTGTACTAAAGTATCATAGATGCTTCACTATTTTATTC -GAATGCCAT 25088
OY 1281 CCTAGAGCAAGAAAGCCCAAGAGCCGAGTCAGATGCTCTGACGCAAGATGTGT 1340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25089 CCTGGGTGGAAGAACCCCAAGAGGACAGACAGCCCTGTCAAGCAAGAGTGTGT 25148
OY 1341 AAGGACAGGCTTGTGATGGCTGGTGGCGGAGCAAAATTCATCCAGCTACTGACAGAT 1400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25149 AAGGACA-----TCATGGCTGTGGTGGGGAATAATTCATCCAGCTACTGACAGC 25204
OY 1401 CATGATCCGCCCCATTGCTTTAAGCCCAAGCAAGTTAAGCAGAGGTTAGAGGTGAA 1460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25205 CATGATCCGCCCCATTGCTTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA 25254
OY 1461 GACGCTGCTTCTCTCTTCCAGAGCAAGTGGACACCTTCTGTGTCTGTGAGAACATG 1520
DB 25255 ----- 25254
OY 1521 AGTGTGACCAATGAGCAGACATGCTGTGACACTTTAGAGTCAAGAGACTGCCAGCAG 1580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25255 -----CAACGACATTCCTCTACTTGTAGGCAAGAGGCTGTGAGCAGG 25259

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OY 1581 G---TTTGTGACAGACGCCCTTACTTTCCGGGACACACCTGAGTGTGAAGGCAAGAAACA 1637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25300 GGGTTTGTAGGGGGAATACCCCTTCTAGGACACCTTGAGGAGTAAGGGCAGACAAACA 25359
OY 1638 GGTGAGGGTGAAGTGTGACACCCAGAGAC--TGCTCTGCGCCCTCACCTGCCCCACTG 1695
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25360 GGTGAGGGTGAAGTGTGACACACAGACTGTCTTCTGCTCCCTCACCTGCCCCACTG 25419
OY 1696 CTACGACTGGAGC-----TGACATGACACGCCCATGATCTGTGACAGAGTCTCT 1746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25420 CCACAACATTTGGCCTTACCTTGGGAGGTGGCATTCACGATCTCTGTGCGCAGGCGCT 25479
OY 1747 GCT-CTGTGCGAGGCTCTTGTATTAAGCATGATGATGATGATGATGATGATGATGATG 1805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25480 GCTACCTGCTAGACTCTTATTAAGCATGATGATGATGATGATGATGATGATGATGATG 25539
OY 1806 CTTGAGACACGACGCTACCTTGTGATGCTGTGTGAGACACAGAGTGTGAGAGCATCTCA 1865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25540 CTTGAGACACGACGCTACCTTGTGATGCTGTGTGAGACACAGAGTGTGAGAGCATCTCA 25599
OY 1866 GGCAGCTCAGCCCAAGCTTCTACCTGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTG 1924
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25600 GGCAGACTAAGCTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTG 25659
OY 1925 ACCAGGTTGGGAATGAGAGATGACATGGCATGTATGAGAGGATGAGAGATTTTCCG 1984
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25660 ACCAGGTTGGGAATGAGAGATGAGAGAT-----GGAGGTGTGAGAGATGAATTTTCATG 25712
OY 1985 AAAAAAAAAAAAAAAAAA 2004
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25713 TAAACTTTTAAAAAGAA 25732

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RESULT 13  
G23637/c 391 bp DNA linear STS 31-MAY-1996  
LOCUS G23637  
DEFINITION human STS WI-13434, sequence tagged site.  
ACCESSION G23637  
VERSION G23637.1 GI:1343963  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens STS derived from sequences in dbEST and the Unigene collection.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 391)  
AUTHORS Hudson,T.  
TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
Mapped STS  
JOURNAL Unpublished (1995)  
COMMENT

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Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: TACATGAATCTTCCATCCTTC  
Primer B: CTGTGACACAGATGCTTGA  
STS size: 150  
PCR Profile:

Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primer: each 5 pm  
dNTPs: each 4 mM



